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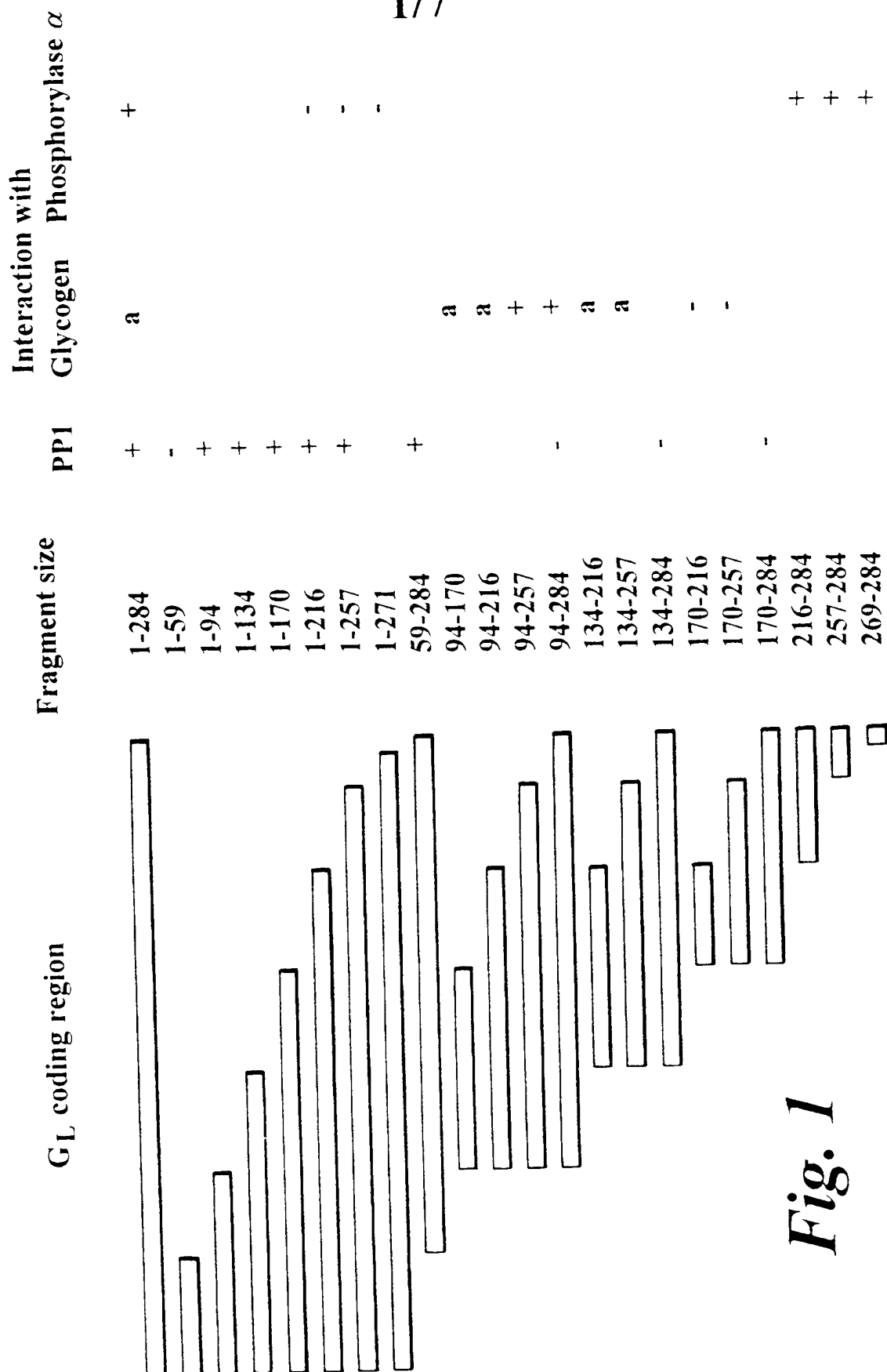
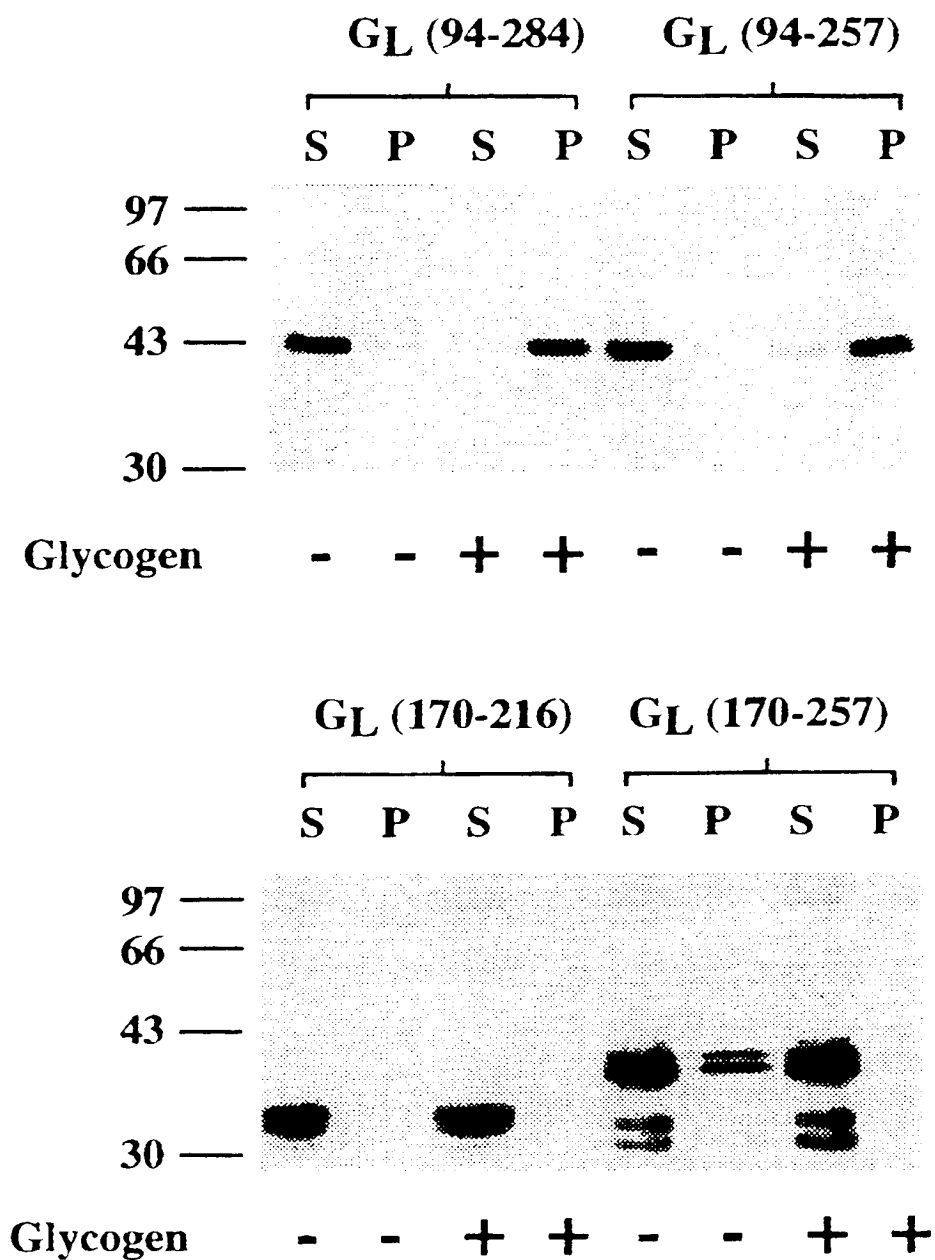
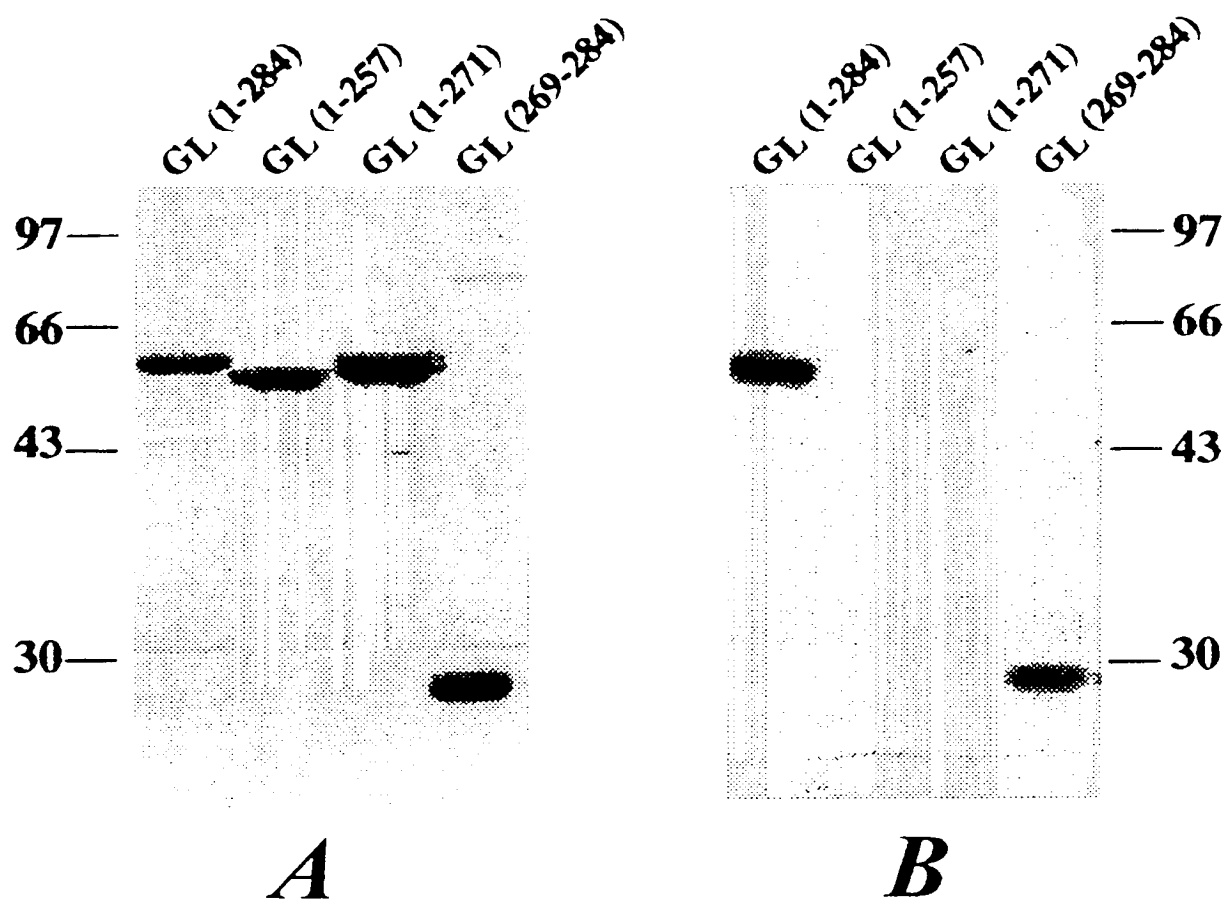


Fig. 1

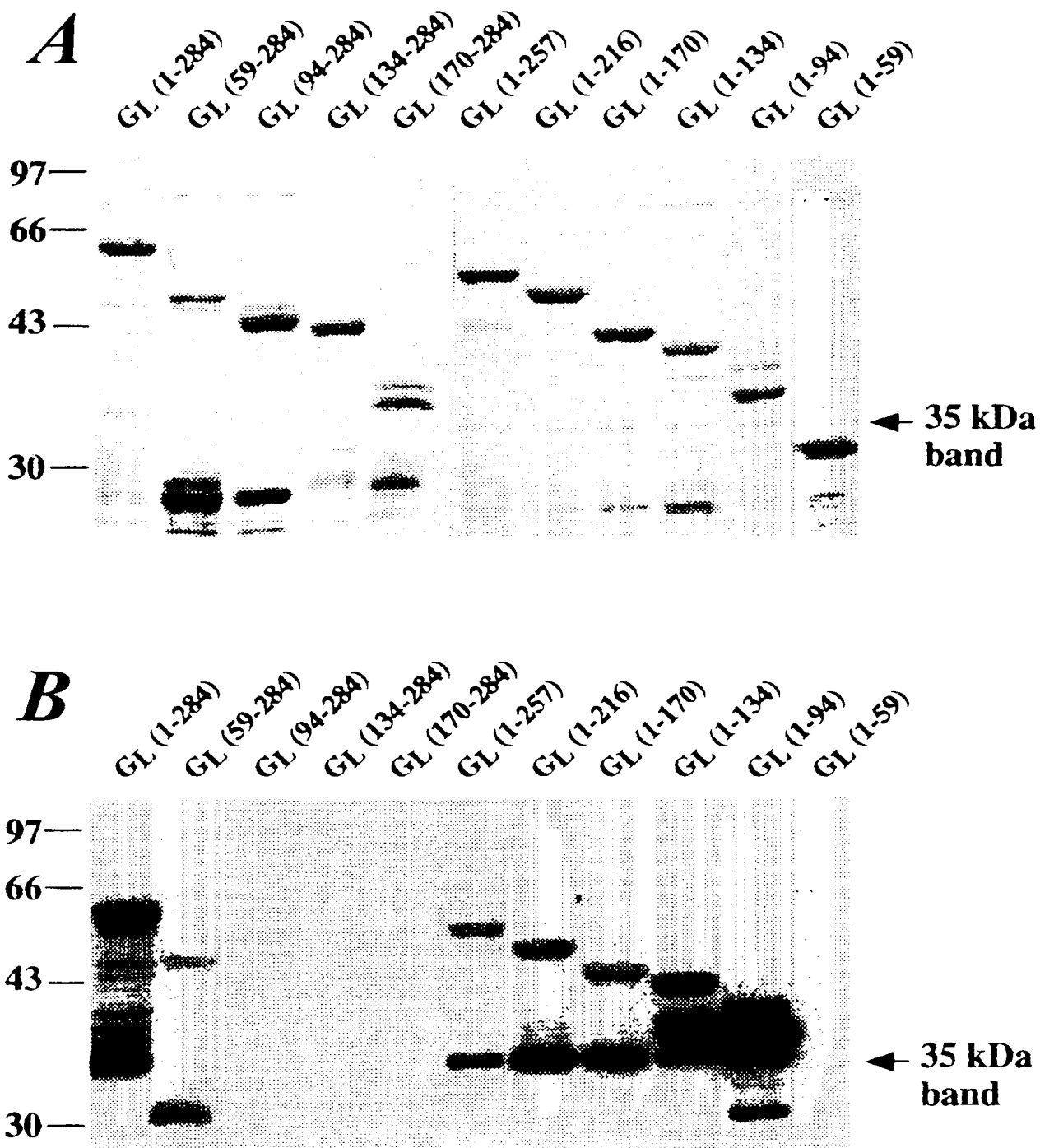
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*Fig. 2*

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*Fig. 3*

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**Fig. 4**

SUBSTITUTE SHEET (RULE 26)

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M ₁₁₀ (1-38)peptide	26	...PPVVK <u>Q</u> <u>R</u> TKVKE	38
G _L	52	...TVQEK <u>K</u> <u>V</u> KRVSFADQGL...	69
G _M (63-93)peptide	63	GRRV <u>S</u> <u>F</u> ADNFG...	73

Fig. 5

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G _L	132	VC <u>LE</u> ---NCVLKEKAIAGTVK <u>VQ</u> NLA <u>FE</u> KVVK <u>IR</u> M--TFDTWKSFT	172
R5	157	VC <u>LE</u> ---NCSLQERTVTGTVK <u>VKN</u> VS <u>FE</u> KKVQIR <u>I</u> --TFDSWKNYT	197
R6	177	VC <u>LE</u> ---RVTCSDLGISGTVRV <u>CN</u> VAF <u>EK</u> QVAVRY--TFSGWRSTH	217
G _M	128	AI <u>LE</u> S-TESLLGSTSIKGI <u>IR</u> VLNV <u>SFE</u> KL <u>VY</u> VRM--SLDDWQTHY	170
GAC1	244	VKLHSLTQLGDDSSK <u>IT</u> GLVYV <u>KN</u> L <u>SFE</u> KYLEIK <u>E</u> --TFNSWRDIH	287
AMYL	33	VQ <u>LD</u> S---YNYDGSTFSGKIYVKNIAYSKKVTVIYADGSDNWNNG	75
Consensus		φ . G . V . V . N φ . F . K . V . V . φ W	
		I Y L I	
PHOS	398	RHLQIIYEINQRFNLNRVAAAFPGDVDRLRRMS	429
		** *** *	
G _L	173	DFPCQYVKDITYAGSDRD <u>TF</u> S <u>FD</u> ISLPEKIQSYE-----	205
R5	198	DVDCVYMKNVYGGTDS <u>DT</u> S <u>FE</u> FAIDLPPVIPTEQ-----	230
R6	218	EAVARWRGPAGPEGTE <u>DV</u> T <u>FG</u> FPVPPFLLELGS-----	251
G _M	171	DILAEYVPNSCDG-ETDQ <u>FE</u> S <u>FK</u> IVLVPPYQKDGS-----	203
GAC1	288	YVTANFNRTIN--SNVDE <u>FK</u> ETID <u>LN</u> SLKYILLIKRIITMEKNTSS	331
AMYL	76	NTIAASYSAPISGSNYEY <u>WT</u> ESAS <u>IN</u> GK-----	104
Consensus		D . F . F . . . φ	
		E W	
PHOS	330	LVEEGAVK	437
		* * *	
G _L	206	---RMEFAVCY <u>EC</u> NGQSYWDSNKGKNY <u>RI</u>	231
R5	231	---KIEFCISYHANGQVFDNNDGQNY <u>RI</u>	256
R6	252	---RVHFAVRYQVAGAEYWDNNDHRDY <u>SL</u>	282
G _M	204	---KVEFCIRYETSVGT <u>FW</u> SNNNGTNY <u>TF</u>	229
GAC1	332	CPLNIELCCRYDVNNETYYDNNGKNY <u>HL</u>	360
AMYL	105	-----EFYIKYEVSCKTYDNNNSANYQV	128
Consensus		F . φ . Y YW . . N Y . φ	
		L FY	

Fig. 6

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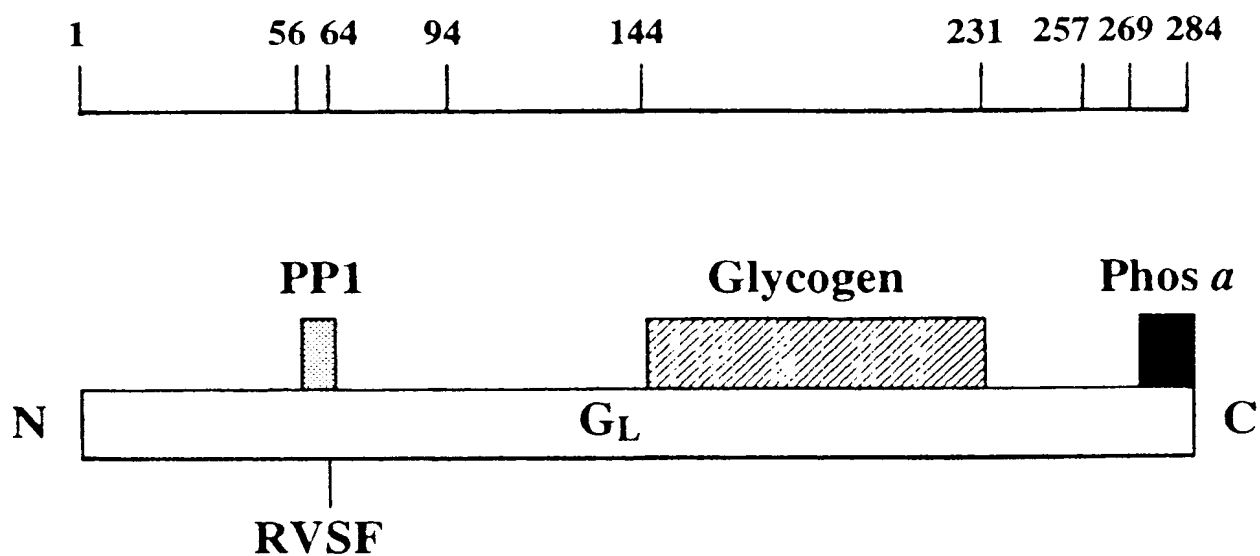


Fig. 7